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TECH CENTER 1600/2900

<110> KEITH, TIM  
LITTLE, RANDALL D.  
EERDEWEGH, PAUL VAN  
DUPUIS, JOSEE  
DEL MASTRO, RICHARD L.  
SIMON, JASON  
ALLEN, KRISTINA  
PANDIT, SUNIL

<120> NOVEL HUMAN GENES RELATING TO RESPIRATORY DISEASES AND OBESITY

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 245 250 255  
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr  
 260 265 270

Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 275 280 285  
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro  
 290 295 300  
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu  
 305 310 315 320  
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala  
 325 330 335  
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg  
 340 345 350  
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp  
 355 360 365  
 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys  
 370 375 380  
 Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro Trp  
 385 390 395 400  
 Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala Pro  
 405 410 415  
 Ala Phe Pro Leu Ser Arg Gln Gly Phe Ser Ser Leu Ala Arg Leu Val  
 420 425 430  
 Ser Asn Ser  
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 <211> 1441  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(1166)

<400> 4  
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 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg  
 1 5 10 15  
 gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95  
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro  
 20 25 30  
 cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct 143  
 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser  
 35 40 45



gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa 191  
 Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu  
 50 55 60

ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc 239  
 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro  
 65 70 75

cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287  
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser  
 80 85 90 95

acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335  
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 100 105 110

gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg 383  
 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr  
 115 120 125

ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431  
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu  
 130 135 140

cag gaa ggg acc ccg gtc cac gaa ctg ccc acg ccc tct cca gga ggg 479  
 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly  
 145 150 155

gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg 527  
 Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly  
 160 165 170 175

tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc ccg gtc cac gaa 575  
 Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu  
 180 185 190

ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca 623  
 Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro  
 195 200 205

cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc 671  
 Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu  
 210 215 220

tcc agg agg gga cac ccg gtt cac gag ctg ccc acg tcc tct cca gga 719  
 Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly  
 225 230 235

ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca 767  
 Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr  
 240 245 250 255

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815  
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser  
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911  
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg  
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959  
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala  
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007  
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala  
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055  
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg  
 340 345 350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103  
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu  
 355 360 365

gac ctg ccc cca tgg acc tgg aga cag ggt ttc tcc tca ttg gcc agg 1151  
 Asp Leu Pro Pro Trp Thr Trp Arg Gln Gly Phe Ser Ser Leu Ala Arg  
 370 375 380

ctg gtc tcg aac tcc tgacctcaga cgatccacct gcctcagcct cccgaagtgt 1206  
 Leu Val Ser Asn Ser  
 385

tgggattaca ggcacgagcc actgtgcccc gccatcattc ctttttactg ctgactaata 1266

gtctgctgtg tgaatccacc gctagaaacc cactcatcag ttgatgggtca tgtgggttgc 1326

ttctgctatt cgcttattat gaacagtgt ggaataaacg ttctgtgca ctcttgggca 1386

tacgcctagg agtggaactg ctgggtcaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1441

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 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
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Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro Arg  
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Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala  
 35 40 45

Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly  
 50 55 60

Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg  
 65 70 75 80  
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr  
 85 90 95  
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 100 105 110  
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro  
 115 120 125  
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln  
 130 135 140  
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp  
 145 150 155 160  
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser  
 165 170 175  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu  
 180 185 190  
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg  
 195 200 205  
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser  
 210 215 220  
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly  
 225 230 235 240  
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro  
 245 250 255  
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr  
 260 265 270  
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 275 280 285  
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro  
 290 295 300  
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu  
 305 310 315 320  
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala  
 325 330 335  
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg  
 340 345 350  
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp  
 355 360 365

Leu Pro Pro Trp Thr Trp Arg Gln Gly Phe Ser Ser Leu Ala Arg Leu  
 370 375 380

Val Ser Asn Ser  
 385

<210> 6  
 <211> 1576  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(1190)

<400> 6  
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 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg  
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 gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95  
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro  
 20 25 30  
 cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct 143  
 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser  
 35 40 45  
 gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa 191  
 Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu  
 50 55 60  
 ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc 239  
 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro  
 65 70 75  
 cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287  
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser  
 80 85 90 95  
 acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335  
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 100 105 110  
 gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg 383  
 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr  
 115 120 125  
 ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431  
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu  
 130 135 140  
 cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg 479  
 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly  
 145 150 155

gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg 527  
 Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly  
 160 165 170 175

tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa 575  
 Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu  
 180 185 190

ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca 623  
 Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro  
 195 200 205

cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc 671  
 Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu  
 210 215 220

tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga 719  
 Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly  
 225 230 235

ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca 767  
 Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr  
 240 245 250 255

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815  
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser  
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911  
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg  
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959  
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala  
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007  
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala  
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055  
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg  
 340 345 350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103  
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu  
 355 360 365

gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga 1151  
 Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly  
 370 375 380

aag gaa ggc tct ggg cat gga gct tta ttg agg tat agt tgacaattca 1200  
 Lys Glu Gly Ser Gly His Gly Ala Leu Leu Arg Tyr Ser  
 385 390 395  
 ggacggtgtg cactcaaggt atgcagcatc acaacctgac acacgtaggc attgtgaaat 1260  
 ggtcccaaca attgggctaa ttaacacacc catcacctta catgggttact tctttctgtg 1320  
 gtgagaacac taaattttta atagaggaca cacagcctgg gcaacatagt gagacctgt 1380  
 ctctacaaat ataaaaaaat tatctggacg tgggtggtgca cacctgtggt cccagctact 1440  
 tgggaagctg aggctggaga atcacttgag cctgggaggc ggaggttgcg gtgcactcca 1500  
 gcctgggcga cagagggagg ccctatctca aaataaataa ataaaggaca cattcttctc 1560  
 aaaaaaaaaa aaaaaa 1576

<210> 7  
 <211> 396  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
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 Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala  
 35 40 45  
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly  
 50 55 60  
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg  
 65 70 75 80  
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr  
 85 90 95  
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 100 105 110  
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro  
 115 120 125  
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln  
 130 135 140  
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp  
 145 150 155 160  
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser  
 165 170 175

Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu  
 180 185 190  
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg  
 195 200 205  
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser  
 210 215 220  
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly  
 225 230 235 240  
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro  
 245 250 255  
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr  
 260 265 270  
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 275 280 285  
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro  
 290 295 300  
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu  
 305 310 315 320  
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala  
 325 330 335  
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg  
 340 345 350  
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp  
 355 360 365  
 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys  
 370 375 380  
 Glu Gly Ser Gly His Gly Ala Leu Leu Arg Tyr Ser  
 385 390 395

<210> 8  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(1244)

<400> 8  
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 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg  
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gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95  
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro  
 20 25 30

cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct 143  
 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser  
 35 40 45

gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa 191  
 Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu  
 50 55 60

ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc 239  
 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro  
 65 70 75

cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287  
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser  
 80 85 90 95

acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335  
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 100 105 110

gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg 383  
 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr  
 115 120 125

ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431  
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu  
 130 135 140

cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg 479  
 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly  
 145 150 155

gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg 527  
 Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly  
 160 165 170 175

tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa 575  
 Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu  
 180 185 190

ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca 623  
 Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro  
 195 200 205

cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc 671  
 Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu  
 210 215 220

tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga 719  
 Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly  
 225 230 235



ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca 767  
 Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr  
 240 245 250 255  
 ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815  
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser  
 260 265 270  
 acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 275 280 285  
 gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911  
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg  
 290 295 300  
 ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959  
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala  
 305 310 315  
 ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007  
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala  
 320 325 330 335  
 gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055  
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg  
 340 345 350  
 cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103  
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu  
 355 360 365  
 gac ctg ccc cca tgg acc tgg atg cca gtg atg cct gag gtc tgc agg 1151  
 Asp Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg  
 370 375 380  
 gca gtg cat acg ctc acc gcc tgg ccg ctc agg agc ctg tgc ttg acc 1199  
 Ala Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr  
 385 390 395  
 ccc aaa tcc gcc ccc caa ctc cct gtt acc ggc tca ctc ctt cca 1244  
 Pro Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro  
 400 405 410  
 tgaggggcct tccccaggga cagccgatgc tctcctgatg gctcctgccc ttgcagagtg 1304  
 ctgccccgcg ctgccccact ggcctggacc ctgcctgag cccctcagg gctctgcgcc 1364  
 acctcaaccc aggcgtttgt tccgcaggaa cctcccggct cttcccactc gggaaaggaa 1424  
 ggctctgggc atggaggtcg gccaggcccc atccccgtac cctggccctt cttcctgctt 1484  
 cctgtttgtc actgccccgg ggcctttgca cctgcattcc ctctctctgt gaggtcctg 1544  
 gggcccggtta cccacgtcac cgtcccagga taccttttct tttctttctc tctctccagc 1604  
 tttattgagg tatagttgac aattcaggac ggtgtgcact caaggtatgc agcatcacia 1664

cctgacacac gtaggcattg tgaaatgagt cccacaattg ggctaattaa cacacccatc 1724  
 accttacatg gttacttctt tctgtggtga gaacactaaa ttttaaatag aggacacaca 1784  
 gcctgggcaa catagtgaga ccctgtctct acaaataaa aaaaattatc tggacgtggt 1844  
 ggtgcacacc tgtggtccca gctacttggg aagctgagggc tggagaatca cttgagcctg 1904  
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 aaataaataa aggacacatt cttatcaaaa aaaaaaaaaa aaaaaa 2010

<210> 9  
 <211> 414  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
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                     20                    25                    30  
 Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala  
                     35                    40                    45  
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly  
                     50                    55                    60  
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg  
                     65                    70                    75                    80  
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr  
                     85                    90                    95  
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
                     100                    105                    110  
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro  
                     115                    120                    125  
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln  
                     130                    135                    140  
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp  
                     145                    150                    155                    160  
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser  
                     165                    170                    175  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu  
                     180                    185                    190  
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg  
                     195                    200                    205

Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser  
 210 215 220  
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly  
 225 230 235 240  
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro  
 245 250 255  
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr  
 260 265 270  
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 275 280 285  
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro  
 290 295 300  
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu  
 305 310 315 320  
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala  
 325 330 335  
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg  
 340 345 350  
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp  
 355 360 365  
 Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg Ala  
 370 375 380  
 Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr Pro  
 385 390 395 400  
 Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro  
 405 410

<210> 10  
 <211> 1744  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (3)..(1349)

<400> 10 47  
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 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg 15  
 1 5 10  
 gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95  
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro 30  
 20 25 30

cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct 143  
 Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser  
                   35                  40                  45

gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa 191  
 Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu  
                   50                  55                  60

ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc 239  
 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro  
                   65                  70                  75

cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287  
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser  
                   80                  85                  90                  95

acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335  
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
                   100                  105                  110

gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg 383  
 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr  
                   115                  120                  125

ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431  
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu  
                   130                  135                  140

cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg 479  
 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly  
                   145                  150                  155

gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg 527  
 Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly  
                   160                  165                  170                  175

tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa 575  
 Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu  
                   180                  185                  190

ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca 623  
 Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro  
                   195                  200                  205

cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc 671  
 Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu  
                   210                  215                  220

tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga 719  
 Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly  
                   225                  230                  235

ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca 767  
 Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr  
                   240                  245                  250                  255

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815  
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser  
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911  
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg  
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959  
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala  
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007  
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala  
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055  
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg  
 340 345 350

cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg 1103  
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu  
 355 360 365

gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga 1151  
 Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly  
 370 375 380

aag gaa ggc tct ggg cat gga ggt cgg cca ggc ccc atc ccc gta ccc 1199  
 Lys Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro  
 385 390 395

tgg ccc ttc ttc ctg ctt cct gtt tgt cac tgc ccc ggg gcc ttt gca 1247  
 Trp Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala  
 400 405 410 415

cct gca ttc cct ctc tct gtg agt gtc ctg ggg ccc gtt acc cac gtc 1295  
 Pro Ala Phe Pro Leu Ser Val Ser Val Leu Gly Pro Val Thr His Val  
 420 425 430

acc gtc cca gga tac ctt ttc ttt tct ttc tct ctc tcc agc ttt att 1343  
 Thr Val Pro Gly Tyr Leu Phe Phe Ser Phe Ser Leu Ser Ser Phe Ile  
 435 440 445

gag gta tagttgacaa ttcaggacgg tgtgcactca aggtatgcag catcacaacc 1399  
 Glu Val

tgacacacgt aggcattgtg aaatgagtcc cacaattggg ctaattaaca caccatcac 1459

cttacatggt tacttctttc tgtggtgaga acactaaatt ttaaataagag gacacacagc 1519

ctgggcaaca tagtgagacc ctgtctctac aaatataaaa aaattatctg gacgtgggtgg 1579

tgacacacctg tgggtcccagc tacttgggaa gctgaggctg gagaatcact tgagcctggg 1639

aggcggaggt tgcggtgcac tccagcctgg ggcacagagg gaggcctat ctcaaaataa 1699  
 ataaataaag gacacattct tatcaaaaaa aaaaaaaaaa aaaaa 1744

<210> 11  
 <211> 449  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala  
 1 5 10 15  
 Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro Arg  
 20 25 30  
 Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala  
 35 40 45  
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly  
 50 55 60  
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg  
 65 70 75 80  
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr  
 85 90 95  
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 100 105 110  
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro  
 115 120 125  
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln  
 130 135 140  
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp  
 145 150 155 160  
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser  
 165 170 175  
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu  
 180 185 190  
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg  
 195 200 205  
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser  
 210 215 220  
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly  
 225 230 235 240

Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro  
 245 250 255  
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr  
 260 265 270  
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala  
 275 280 285  
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro  
 290 295 300  
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu  
 305 310 315 320  
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Gly Ala Gly Ser Pro Ala Ala  
 325 330 335  
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg  
 340 345 350  
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp  
 355 360 365  
 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys  
 370 375 380  
 Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro Trp  
 385 390 395 400  
 Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala Pro  
 405 410 415  
 Ala Phe Pro Leu Ser Val Ser Val Leu Gly Pro Val Thr His Val Thr  
 420 425 430  
 Val Pro Gly Tyr Leu Phe Phe Ser Phe Ser Leu Ser Ser Phe Ile Glu  
 435 440 445  
 Val

<210> 12  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 12  
 gtagtaacag aatggacttt ga

<210> 13  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
agagaggaac agcatcaaag tc 22

<210> 14  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
caaacagggt ccaccgtgga aa 22

<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
gtgtttcagc cacatttcca cg 22

<210> 16  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
atccaccgct agaaaccac tc 22

<210> 17  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
gaccatcaac tgatgagtgg gt 22

<210> 18  
<211> 22



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
tcatgggggt gctttgacct tg 22

<210> 19  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19  
tggcctcaaa ggctcaaggt ca 22

<210> 20  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20  
tgtaggacta tattgctc 18

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21  
cgacatttag gtgacact 18

<210> 22  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic adapter  
oligonucleotide

<400> 22  
gtcttcacca cgggg 15

<210> 23  
<211> 11  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic adapter  
oligonucleotide

<400> 23  
gtggtgaaga c 11

<210> 24  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
gcccttaggg agagcagc 18

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
ccacatcggtg cctttgtgta 20

<210> 26  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
cactgtgtta aaacgcctgg 20

<210> 27  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
gttgggatta caggcacgag

20

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 28  
cagaagcaac ccacatgacc

20

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 29  
actacaggtt tgcaccacca

20

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 30  
atgctctcct gatggctcct

20

<210> 31  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 31  
agggaatgca ggtgcaaag

19

<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 32  
 actcgggaaa ggaaggctct 20

<210> 33  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
 cataccttga gtgcacaccg 20

<210> 34  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 34  
 gacagtctgc tccacatcca 20

<210> 35  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 35  
 tggagatgaa gtcttgctct tg 22

<210> 36  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 36  
 atatgtttgc tggctttggg 20

<210> 37  
 <211> 20

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 37  
 cccaggctgt gtgtcctcta

20

<210> 38  
 <211> 1124  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
 tcacgagctg cccacgtcct ctccaggaag ggaccccggtg ttcacgagct gcccacgtcg 60  
 tctccaggaa gggacccggg tccacgagct gcccacgtcc tctccaggaa aggacccggg 120  
 tccacgagct ggccacgtcc tctgcaggaa gggaccccggtg gtccacgagc tgccacgtc 180  
 ctctccagga agggaccccg gggttcacgag ctgcccacgt cctctccagg aaggggaccc 240  
 ggggtccacga gctgcccacg tctctccag gaagggaccc cgggtccacg aactgcccac 300  
 gtctctcca ggaagggaacc ccgggttcac gagctgccc cgtcctctcc aggaggggac 360  
 accgggttca cgagctgccc acgcccctct caggaaggga ccccggttc atgagctgcc 420  
 cagtcctct ccaggaaggg acccggttcc acgaactgcc cagcccctct ccaggagggg 480  
 acccggttcc acgagctgcc cagtcgtca acgggaaggg acccggttcc acgagctgcc 540  
 cagtcctct ccaggaaggg acccggttcc acgaactgcc cagcgcctct ccaggagggg 600  
 acacgggtt cagcagctgc ccacgcctc tccaggaagg gaccccggtt tcacgagctg 660  
 cccacgtcct ctccaggagg ggacacccggg ttcacgagct gcccacgtcc tctccaggag 720  
 gggacaccgg gttcacgagc tgcccacgcc ctctccagga ggggacaccg ggttcacgag 780  
 ctgcccacgt cctctccagg aagggaaccg ggtccacgag ctgcccacgt cctctccagg 840  
 aggggacacc ggggttcacga gctgcccacg cactttccag gaagggaccc cgggttcagg 900  
 tctctgccc gcccacatcg tgctttgtg taaatcagaa gaaagatgag gaacaggccc 960  
 tctctctct ccaggcaggc tttgggtggag gggctggatc tctgcccga ccttccctgg 1020  
 cagggcaccc tgtgcttgag ccccgagaact gcaggcggcc ggcagagaag ggggtccatga 1080  
 tggcgctcg gtgcgcagcc ttggacctgc ccccatggac ctgg 1124

<210> 39  
 <211> 289  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 agacagggtt tctcctcatt ggccaggctg gtctcgaact cctgacctca gacgatccac 60  
 ctgcctcagc ctcccgaagt gttgggatta caggcagcag ccactgtgcc cggccatcat 120  
 tcttttttac tgctgactaa tagtctgctg tgtgaatcca ccgctagaaa cccactcatc 180  
 agttgatggg catgtgggtt gcttctgcta ttcgcttatt atgaacagtg ctggaataaa 240  
 cgttcctgtg cactcttggg catacgcta ggagtggaa tgctgggtc 289

<210> 40  
 <211> 139  
 <212> DNA  
 <213> Homo sapiens

<400> 40  
 gaacctcccg gctcttccca ctccgggaaag gaaggctctg ggcattggagg tcggccaggc 60  
 cccatccccc taccctggcc cttcttctct cttctgttt gtcactgcc cgggagcctt 120

gcacctgcat tccctctct

139

<210> 41  
 <211> 49  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 gaacctcccg gctcttccca ctccgggaaag gaaggctctg ggcattggag

49

<210> 42  
 <211> 866  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 tgagggggcct tccccaggga cagccgatgc tctcctgatg gctcctgccc ttgcagagtg 180  
 ctgccccgcg ctgccacact ggccctggacc ctccgctgag cccctcagg gctctgcgcc 240  
 acctcaaccc aggcgtttgt tccgcaggaa cctcccggtc cttccactc gggaaaggaa 300  
 ggctctgggc atggaggtcg gccaggcccc atccccgtac cctggccctt cttcctgctt 360  
 cctgtttgtc actgccccgg ggccctttgca cctgcattcc ctctctctgt gagggtcctg 420  
 gggcccggtta cccacgtcac cgtcccaggga taccttttct tttctttctc tctctccagc 480  
 tttattgagg tatagttgac aattcaggac ggtgtgcact caaggatgac agcatcaca 540  
 cctgacacac gtaggcattg tgaaatgagt cccacaattg ggctaattaa cacacccatc 600  
 accttacatg gttacttctt tctgtggtga gaacactaaa ttttaaatag aggacacaca 660  
 gcctgggcaa catagtgaga ccctgtctct acaaatataa aaaaattatc tggacgtggg 720  
 ggtgcacacc tgtggtccca gctacttggg aagctgaggc tggagaatca cttgagcctg 780  
 ggaggcgag gttgcggtgc actccagcct gggcgacaga gggaggccct atctcaaaat 840  
 aaataaataa aggacacatt cttatc 866

<210> 43  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 ctttattgag gtatagttga caattcaggga cgggtgtgcac tcaagggtatg cagcatcaca 60  
 acctgacaca cgtaggcatt gtgaaatgag tcccacaatt gggctaatta acacacccat 120  
 caccctacat gggtacttct ttctgtggtg agaacactaa attttaaata gaggacacac 180  
 agcctgggca acatagtgag accctgtctc tacaaatata aaaaaattat ctggacgtgg 240  
 tgggtgcacac ctgtggtccc agctacttgg gaagctgagg ctggagaatc acttgagcct 300  
 gggaggcgga ggttgcggtg cactccagcc tggcgacaga agggaggccc tatctcaaaa 360  
 taaataaata aaggacacat tcttatc 387

<210> 44  
 <211> 599  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
 gaacctcccg gctcttccca ctccgggaaag gaaggctctg ggcattggag tccggccaggc 60  
 cccatccccc taccctggcc cttcttctctg cttcctgttt gtcactgccc cggggccttt 120

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gcacctgcat tccctctctc tgtgagtgtc ctggggcccg ttacccacgt caccgtcca 180
ggataccttt tcttttcttt ctctctctcc agctttattg aggtatagtt gacaattcag 240
gacgggtgtgc actcaaggta tgcagcatca caacctgaca cacgtaggca ttgtgaaatg 300
agtcccacaa ttgggctaata taacacaccc atcaccttac atgggtactt ctttctgtgg 360
tgagaacact aaatttttaa tagaggacac acagcctggg caacatagtg agaccctgtc 420
tctacaaata taaaaaaatt atctggacgt ggtgggtgcac acctgtggtc ccagctactt 480
gggaagctga ggctggagaa tcacttgagc ctgggaggcg gaggttgcgg tgcactccag 540
cctgggcgac agagggaggc cctatctcaa aataaataaa taaaggacac attcttattc 599

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<210> 45
<211> 1028
<212> DNA
<213> Homo sapiens

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<220>
<221> modified_base
<222> (267)
<223> a, t, c or g

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<400> 45
cgggcgtgta tatctcttca tagagagcgc tcagacagcg tgcgttaatc tgcgtcgata 60
tatagagatc tttatcactg agtagataga acgtacatga atgtacgaac agtccagacg 120
agtaacttga ctaggataag atagacagta ccaactaatg agacaagaag agggaaatcat 180
atagaatcat gtagtctgag tctagcgagt gtcgacatga tcacaagcga aatacagact 240
atgagaagag gtagaaataa taagtanact gagaagagag gtcatatgta catacaaatc 300
agtaaagcaa tagaaattga atacattata agccacagtt acagaattag cctaatttaa 360
caacatggc aagcgagtta tatcaaacat agaagagtaa actctatcga ccatgggtag 420
gaacgaataa aggcgtcgag aagacaataa gaatgcgtgt taaacagcaa tacaagagaa 480
tagcaccact gaagcagacc aaaggcgtca ccgggggaagt aggggaagagg cacctcaca 540
ggagaggaaa gggcagtcct gattttgaaa atttcagtga aaagacagtg ttgttccgg 600
aggcagctta gtgatcccg atcgactctg aagaggaccc tgagggtagg ggatttttgg 660
gcttgaccgg cctatgctga acgcccaccg ggaattcagg gagaaacacg gggcccggc 720
ttccaggaga gcagccaggc cacagccctg aggacgggca aaccccaccc aggcacgggtg 780
agagggaggc cgcccaggcc tggggcctgg cggcagggga tgaagtggac cagagccccg 840
caaatacctaa cgtgggtgag cagtgagcct gtgtggctgc gagtggctcc gttttggggc 900
tgtttgttcc tgcagcaaat gatgccagcc ctgacgggaa cagtgcacgt ccaccacgag 960
ctgcccacgt cctctccagg aagggaaccc ggccacagag ctgcccacgt cctctccagg 1020
aagggacc 1028

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<210> 46
<211> 40
<212> DNA
<213> Homo sapiens

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<400> 46
actacagggt tgcaccacca tgcctgcta attttttttt 40

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<210> 47
<211> 40
<212> DNA
<213> Homo sapiens

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<400> 47
actacagggt tgcaccaccg tgcctgcta attttttttt 40

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<210> 48  
<211> 39  
<212> DNA  
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